



RECEIVED

SEP 30 2002

SEQUENCE LISTING

TECH CENTER 1600/2900

<10> Kaufman, Randal J.
Tirasophon, Witoon
Welihinda, Ajith A.

<120> Irelp, A NOVEL MAMMALIAN PROTEIN AND GENE ENCODING SAME

<130> UMV-1584

<140> US 09/357,273

<141> 1999-07-20

<150> US 60/093,526

<151> 1998-07-21

<160> 13

<170> PatentIn Ver. 2.0

<210> 1

<211> 3629

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (97)..(3027)

<400> 1

ccggctcgac ggctcgggtca ccgcctcgcgt gtcgctgcgcg cgcccccggc cgtcctctgt 60

ccgtaccgcc cccggagcca gggccgagtc ctgcgc atg ccg gcc cgg cgg ctg 114
Met Pro Ala Arg Arg Leu
1 5

ctg ctg ctg ctg acg ctg ctg ctg ccc ggc ctc ggg att ttt gga agt 162
Leu-Leu-Leu-Leu-Thr Leu-Leu-Leu-Pro Gly-Leu-Gly-Ile-Phe-Gly-Ser-
10 15 20

acc agc aca gtg acg ctt cct gaa acc ttg ttg ttt gtg tca acg ctg 210
Thr Ser Thr Val Thr Leu Pro Glu Thr Leu Leu Phe Val Ser Thr Leu
25 30 35

gat gga agt ttg cat gct gtc agc aag agg aca ggc tca atc aaa tgg 258
Asp Gly Ser Leu His Ala Val Ser Lys Arg Thr Gly Ser Ile Lys Trp
40 45 50

act tta aaa gaa gat cca gtc ctg cag gtc cca aca cat gtg gaa gag 306
Thr Leu Lys Glu Asp Pro Val Leu Gln Val Pro Thr His Val Glu Glu
55 60 65 70

cct gcc ttt ctc cca gat cct aat gat ggc agc ctg tat acg ctt gga 354
Pro Ala Phe Leu Pro Asp Pro Asn Asp Gly Ser Leu Tyr Thr Leu Gly
75 80 85

agc aag aat aat gaa ggc ctg acg aaa ctt cct ttt acc atc cca gaa 402
Ser Lys Asn Asn Glu Gly Leu Thr Lys Leu Pro Phe Thr Ile Pro Glu
90 95 100

ttg gtg cag gca tcc cca tgc cga agt tca gat gga atc ctc tac atg 450

Leu	Val	Gln	Ala	Ser	Pro	Cys	Arg	Ser	Ser	Asp	Gly	Ile	Leu	Tyr	Met		
		105					110					115					
ggt	aaa	aag	cag	gac	atc	tgg	tat	gtt	att	gac	ctc	ctg	acc	gga	gag	498	
Gly	Lys	Lys	Gln	Asp	Ile	Trp	Tyr	Val	Ile	Asp	Leu	Leu	Thr	Gly	Glu		
	120					125					130						
aag	cag	cag	act	ttg	tca	tcg	gcc	ttt	gca	gat	agt	ctc	tgc	cca	tca	546	
Lys	Gln	Gln	Thr	Leu	Ser	Ser	Ala	Phe	Ala	Asp	Ser	Leu	Cys	Pro	Ser		
135					140					145					150		
acc	tct	ctt	ctg	tat	ctt	ggg	cga	aca	gaa	tac	acc	atc	acc	atg	tac	594	
Thr	Ser	Leu	Leu	Tyr	Leu	Gly	Arg	Thr	Glu	Tyr	Thr	Ile	Thr	Met	Tyr		
				155					160					165			
gac	acc	aaa	acc	cga	gag	ctc	cgg	tgg	aat	gcc	acc	tac	ttt	gac	tat	642	
Asp	Thr	Lys	Thr	Arg	Glu	Leu	Arg	Trp	Asn	Ala	Thr	Tyr	Phe	Asp	Tyr		
			170					175					180				
gcg	gcc	tca	ctg	cct	gag	gac	gaa	ggg	gac	tac	aag	atg	tcc	cac	ttt	690	
Ala	Ala	Ser	Leu	Pro	Glu	Asp	Glu	Gly	Asp	Tyr	Lys	Met	Ser	His	Phe		
		185					190					195					
gtg	tcc	aat	ggt	gat	ggg	ctg	gtg	gtg	act	gtg	gac	agt	gaa	tct	ggg	738	
Val	Ser	Asn	Gly	Asp	Gly	Leu	Val	Val	Thr	Val	Asp	Ser	Glu	Ser	Gly		
	200					205					210						
gac	gtc	ctg	tgg	atc	caa	aac	tac	gcc	tcc	cct	gtg	gtg	gcc	ttt	tat	786	
Asp	Val	Leu	Trp	Ile	Gln	Asn	Tyr	Ala	Ser	Pro	Val	Val	Ala	Phe	Tyr		
215					220					225					230		
gtc	tgg	cag	cgg	gag	ggt	ctg	agg	aag	gtg	atg	cac	atc	aat	gtc	got	834	
Val	Trp	Gln	Arg	Glu	Gly	Leu	Arg	Lys	Val	Met	His	Ile	Asn	Val	Ala		
				235					240					245			
gtg	gag	acc	ctg	cgc	tat	ctg	acc	ttc	atg	tct	ggg	gag	gtg	ggg	cgc	882	
Val	Glu	Thr	Leu	Arg	Tyr	Leu	Thr	Phe	Met	Ser	Gly	Glu	Val	Gly	Arg		
			250					255					260				
atc	aca	aag	tgg	aag	tac	ccg	ttc	ccc	aag	gag	aca	gag	gcc	aag	agc	930	
Ile	Thr	Lys	Trp	Lys	Tyr	Pro	Phe	Pro	Lys	Glu	Thr	Glu	Ala	Lys	Ser		
		265					270					275					
aag	ctg	acg	ccc	act	ctg	tat	gtt	ggg	aaa	tac	tct	acc	agc	ctc	tat	978	
Lys	Leu	Thr	Pro	Thr	Leu	Tyr	Val	Gly	Lys	Tyr	Ser	Thr	Ser	Leu	Tyr		
	280					285					290						
gcc	tct	ccc	tca	atg	gta	cac	gag	ggg	gtt	gct	gtc	gtg	ccc	cgc	ggc	1026	
Ala	Ser	Pro	Ser	Met	Val	His	Glu	Gly	Val	Ala	Val	Val	Pro	Arg	Gly		
295					300				305						310		
agc	aca	ctt	cct	ttg	ctg	gaa	ggg	ccc	cag	act	gat	ggc	gtc	acc	atc	1074	
Ser	Thr	Leu	Pro	Leu	Leu	Glu	Gly	Pro	Gln	Thr	Asp	Gly	Val	Thr	Ile		
				315				320						325			
ggg	gac	aag	ggg	gag	tgt	gtg	atc	acg	ccc	agc	acg	gac	gtc	aag	ttt	1122	
Gly	Asp	Lys	Gly	Glu	Cys	Val	Ile	Thr	Pro	Ser	Thr	Asp	Val	Lys	Phe		
			330					335					340				
gat	ccc	gga	ctc	aaa	agc	aag	aac	aag	ctc	aac	tac	ttg	agg	aat	tac	1170	
Asp	Pro	Gly	Leu	Lys	Ser	Lys	Asn	Lys	Leu	Asn	Tyr	Leu	Arg	Asn	Tyr		

C4
Cont

345	350	355	
tgg ctt ctg ata gga cac cat gaa acc cca ctg tct gcg tct acc aag Trp Leu Leu Ile Gly His His Glu Thr Pro Leu Ser Ala Ser Thr Lys 360 365 370			1218
atg ctg gag aga ttt ccc aac aat cta ccc aaa cat cgg gaa aat gtg Met Leu Glu Arg Phe Pro Asn Asn Leu Pro Lys His Arg Glu Asn Val 375 380 385 390			1266
att cct gct gat tca gag aaa aag agc ttt gag gaa gtt atc aac ctg Ile Pro Ala Asp Ser Glu Lys Lys Ser Phe Glu Glu Val Ile Asn Leu 395 400 405			1314
gtt gac cag act tca gaa aac gca cct acc acc gtg tct cgg gat gtg Val Asp Gln Thr Ser Glu Asn Ala Pro Thr Thr Val Ser Arg Asp Val 410 415 420			1362
gag gag aag ccc gcc cat gcc cct gcc cgg ccc gag gcc ccc gtg gac Glu Glu Lys Pro Ala His Ala Pro Ala Arg Pro Glu Ala Pro Val Asp 425 430 435			1410
tcc atg ctt aag gac atg gct acc atc atc ctg agc acc ttc ctg ctg Ser Met Leu Lys Asp Met Ala Thr Ile Ile Leu Ser Thr Phe Leu Leu 440 445 450			1458
att ggc tgg gtg gcc ttc atc atc acc tat ccc ctg agc atg cat cag Ile Gly Trp Val Ala Phe Ile Ile Thr Tyr Pro Leu Ser Met His Gln 455 460 465 470			1506
cag cag cag ctc cag cac cag cag ttc cag aag gaa ctg gag aag atc Gln Gln Gln Leu Gln His Gln Gln Phe Gln Lys Glu Leu Glu Lys Ile 475 480 485			1554
cag ctc ctg cag cag cag cag cag cag ctg ccc ttc cac cca cct gga Gln Leu Leu Gln Gln Gln Gln Gln Gln Leu Pro Phe His Pro Pro Gly 490 495 500			1602
gac acg gct cag gac ggc gag ctc ctg gac acg tct ggc ccg tac tca Asp Thr Ala Gln Asp Gly Glu Leu Leu Asp Thr Ser Gly Pro Tyr Ser 505 510 515			1650
gag agc tcg ggc acc agc agc ccc agc acg tcc ccc agg gcc tcc aac Glu Ser Ser Gly Thr Ser Ser Pro Ser Thr Ser Pro Arg Ala Ser Asn 520 525 530			1698
cac tcg ctc tgc tcc ggc agc tct gcc tcc aag gct ggc agc agc ccc His Ser Leu Cys Ser Gly Ser Ser Ala Ser Lys Ala Gly Ser Ser Pro 535 540 545 550			1746
tcc ctg gaa caa gac gat gga gat gag gaa acc agc gtg gtg ata gtt Ser Leu Glu Gln Asp Asp Gly Asp Glu Glu Thr Ser Val Val Ile Val 555 560 565			1794
ggg aaa att tcc ttc tgt ccc aag gat gtc ctg ggc cat gga gct gag Gly Lys Ile Ser Phe Cys Pro Lys Asp Val Leu Gly His Gly Ala Glu 570 575 580			1842
ggc aca att gtg tac cgg ggc atg ttt gac aac cgc gac gtg gcc gtg Gly Thr Ile Val Tyr Arg Gly Met Phe Asp Asn Arg Asp Val Ala Val 585 590 595			1890

C⁴
Cont'

aag agg atc ctc ccc gag tgt ttt agc ttc gca gac cgt gag gtc cag Lys Arg Ile Leu Pro Glu Cys Phe Ser Phe Ala Asp Arg Glu Val Gln 600 605 610	1938
ctg ttg cga gaa tcg gat gag cac ccg aac gtg atc cgc tac ttc tgc Leu Leu Arg Glu Ser Asp Glu His Pro Asn Val Ile Arg Tyr Phe Cys 615 620 625 630	1986
acg gag aag gac cgg caa ttc cag tac att gcc atc gag ctg tgt gca Thr Glu Lys Asp Arg Gln Phe Gln Tyr Ile Ala Ile Glu Leu Cys Ala 635 640 645	2034
gcc acc ctg caa gag tat gtg gag cag aag gac ttt gcg cat ctc ggc Ala Thr Leu Gln Glu Tyr Val Glu Gln Lys Asp Phe Ala His Leu Gly 650 655 660	2082
ctg gag ccc atc acc ttg ctg cag cag acc acc tcg ggc ctg gcc cac Leu Glu Pro Ile Thr Leu Leu Gln Gln Thr Thr Ser Gly Leu Ala His 665 670 675	2130
ctc cac tcc ctc aac atc gtt cac aga gac cta aag cca cac aac atc Leu His Ser Leu Asn Ile Val His Arg Asp Leu Lys Pro His Asn Ile 680 685 690	2178
ctc ata tcc atg ccc aat gca cac ggc aag atc aag gcc atg atc tcc Leu Ile Ser Met Pro Asn Ala His Gly Lys Ile Lys Ala Met Ile Ser 695 700 705 710	2226
gac ttt ggc ctc tgc aag aag ctg gca gtg ggc aga cac agt ttc agc Asp Phe Gly Leu Cys Lys Lys Leu Ala Val Gly Arg His Ser Phe Ser 715 720 725	2274
cgc cga tct ggg gtg cct ggc aca gaa ggc tgg atc gct cca gag atg Arg Arg Ser Gly Val Pro Gly Thr Glu Gly Trp Ile Ala Pro Glu Met 730 735 740	2322
ctg agc gaa gac tgt aag gag aac cct acc tac acg gtg gac atc ttt Leu Ser Glu Asp Cys Lys Glu Asn Pro Thr Tyr Thr Val Asp Ile Phe 745 750 755	2370
tct gca ggc tgc gtc ttt tac tac gtg gtc tct gag ggc agc cac cct Ser Ala Gly Cys Val Phe Tyr Tyr Val Val Ser Glu Gly Ser His Pro 760 765 770	2418
ttt ggc aag tcc ctg cag cgg cag gcc aac atc ctc ctg ggt gcc tgc Phe Gly Lys Ser Leu Gln Arg Gln Ala Asn Ile Leu Leu Gly Ala Cys 775 780 785 790	2466
agc ctt gac tgc ttg cac cca gag aag cac gaa gac gtc att gca cga Ser Leu Asp Cys Leu His Pro Glu Lys His Glu Asp Val Ile Ala Arg 795 800 805	2514
gaa ttg ata gag aag atg att gcg atg gat cct cag aaa cgc ccc tca Glu Leu Ile Glu Lys Met Ile Ala Met Asp Pro Gln Lys Arg Pro Ser 810 815 820	2562
gcg aac gac gtg ctc aaa cac ccg ttc ttc tgg agc cta gag aag cag Ala Asn Asp Val Leu Lys His Pro Phe Phe Trp Ser Leu Glu Lys Gln 825 830 835	2610

C4
Cont

ctc cag ttc ttc cag gac gtg agc gac aga ata gaa aag gaa tcc ctg 2658
 Leu Gln Phe Phe Gln Asp Val Ser Asp Arg Ile Glu Lys Glu Ser Leu
 840 845 850

gat ggc ccg atc gtg aag cag tta gag aga ggc ggg aga gcc gtg gtg 2706
 Asp Gly Pro Ile Val Lys Gln Leu Glu Arg Gly Gly Arg Ala Val Val
 855 860 865 870

aag atg gac tgg cgg gag aac atc act gac ccc ctc cag aca gac ctg 2754
 Lys Met Asp Trp Arg Glu Asn Ile Thr Asp Pro Leu Gln Thr Asp Leu
 875 880 885

cgt aaa ttc agg acc tat aaa ggt ggt tct gtc aga gat ctc ctc cga 2802
 Arg Lys Phe Arg Thr Tyr Lys Gly Gly Ser Val Arg Asp Leu Leu Arg
 890 895 900

gcc atg aga aat aag aag cac cac tac cgg gag ctg cct gca gag gtg 2850
 Ala Met Arg Asn Lys Lys His His Tyr Arg Glu Leu Pro Ala Glu Val
 905 910 915

cgg gag acg ctg ggg acc ctc ccc gac gac ttc gtg tgc tac ttc acg 2898
 Arg Glu Thr Leu Gly Thr Leu Pro Asp Asp Phe Val Cys Tyr Phe Thr
 920 925 930

tct cgc ttc ccc cac ctc ctc gca cac acc tac cgg gcc atg gag ctg 2946
 Ser Arg Phe Pro His Leu Leu Ala His Thr Tyr Arg Ala Met Glu Leu
 935 940 945 950

tgc agc cac gag aga ctc ttc cag ccc tac tac ttc cac gag ccc cca 2994
 Cys Ser His Glu Arg Leu Phe Gln Pro Tyr Tyr Phe His Glu Pro Pro
 955 960 965

gag ccc cag ccc cca gtg act cca gac gcc ctc tgagcgaggg cgccccctct 3047
 Glu Pro Gln Pro Pro Val Thr Pro Asp Ala Leu
 970 975

gttctggtgg cccagctgt gactgagggc ctggtcacca caattagagc ttgatgcctc 3107

ccggctttgc agggagacca ggcttcccaa accaagtgcc ttgagctgcc tgctctgcag 3167

cccacagagg acagtgtctga cccaggaag tgggagaagt ggccccctcgt gacctacagg 3227

gaactgggaa gatgctggcc ccaaaagcct tacggtcatg atgtctgcaa aggagggcct 3287

cagagacagc gcgagtagca cccccagcca tctactggat aaacttgctt cagacttttt 3347

aaattcctgc ttaatgtcag tctacaggcc tttcaggaag ggagaggagg gaatcgtaca 3407

ttttgcttgc gtgctgggac agctaggctg agatgcacca agtacagcct tcaactggaga 3467

ccggaattga gaggtggggg atgctgagga gggggaggac ggagttcaga ggggtgtcgtc 3527

ctgcagtatg agattttctca ttgatcacag atgtgcccag agtagcccag gtcactgtta 3587

actagtgttt ctgcagaggc agcaggagcc agccccgaat tc 3629

<210> 2

<211> 977

<212> PRT

C4
Cont'

<213> Homo sapiens

<400> 2

Met Pro Ala Arg Arg Leu Leu Leu Leu Leu Thr Leu Leu Leu Pro Gly
 1 5 10 15
 Leu Gly Ile Phe Gly Ser Thr Ser Thr Val Thr Leu Pro Glu Thr Leu
 20 25 30
 Leu Phe Val Ser Thr Leu Asp Gly Ser Leu His Ala Val Ser Lys Arg
 35 40 45
 Thr Gly Ser Ile Lys Trp Thr Leu Lys Glu Asp Pro Val Leu Gln Val
 50 55 60
 Pro Thr His Val Glu Glu Pro Ala Phe Leu Pro Asp Pro Asn Asp Gly
 65 70 75 80
 Ser Leu Tyr Thr Leu Gly Ser Lys Asn Asn Glu Gly Leu Thr Lys Leu
 85 90 95
 Pro Phe Thr Ile Pro Glu Leu Val Gln Ala Ser Pro Cys Arg Ser Ser
 100 105 110
 Asp Gly Ile Leu Tyr Met Gly Lys Lys Gln Asp Ile Trp Tyr Val Ile
 115 120 125
 Asp Leu Leu Thr Gly Glu Lys Gln Gln Thr Leu Ser Ser Ala Phe Ala
 130 135 140
 Asp Ser Leu Cys Pro Ser Thr Ser Leu Leu Tyr Leu Gly Arg Thr Glu
 145 150 155 160
 Tyr Thr Ile Thr Met Tyr Asp Thr Lys Thr Arg Glu Leu Arg Trp Asn
 165 170 175
 Ala Thr Tyr Phe Asp Tyr Ala Ala Ser Leu Pro Glu Asp Glu Gly Asp
 180 185 190

Tyr Lys Met Ser His Phe Val Ser Asn Gly Asp Gly Leu Val Val Thr
 195 200 205
 Val Asp Ser Glu Ser Gly Asp Val Leu Trp Ile Gln Asn Tyr Ala Ser
 210 215 220
 Pro Val Val Ala Phe Tyr Val Trp Gln Arg Glu Gly Leu Arg Lys Val
 225 230 235 240
 Met His Ile Asn Val Ala Val Glu Thr Leu Arg Tyr Leu Thr Phe Met
 245 250 255
 Ser Gly Glu Val Gly Arg Ile Thr Lys Trp Lys Tyr Pro Phe Pro Lys
 260 265 270
 Glu Thr Glu Ala Lys Ser Lys Leu Thr Pro Thr Leu Tyr Val Gly Lys
 275 280 285
 Tyr Ser Thr Ser Leu Tyr Ala Ser Pro Ser Met Val His Glu Gly Val
 290 295 300
 Ala Val Val Pro Arg Gly Ser Thr Leu Pro Leu Leu Glu Gly Pro Gln

C4
 Cont.

305 310 315 320
 Thr Asp Gly Val Thr Ile Gly Asp Lys Gly Glu Cys Val Ile Thr Pro
 325 330 335
 Ser Thr Asp Val Lys Phe Asp Pro Gly Leu Lys Ser Lys Asn Lys Leu
 340 345 350
 Asn Tyr Leu Arg Asn Tyr Trp Leu Leu Ile Gly His His Glu Thr Pro
 355 360 365
 Leu Ser Ala Ser Thr Lys Met Leu Glu Arg Phe Pro Asn Asn Leu Pro
 370 375 380
 Lys His Arg Glu Asn Val Ile Pro Ala Asp Ser Glu Lys Lys Ser Phe
 385 390 395 400
 Glu Glu Val Ile Asn Leu Val Asp Gln Thr Ser Glu Asn Ala Pro Thr
 405 410 415
 Thr Val Ser Arg Asp Val Glu Glu Lys Pro Ala His Ala Pro Ala Arg
 420 425 430
 Pro Glu Ala Pro Val Asp Ser Met Leu Lys Asp Met Ala Thr Ile Ile
 435 440 445
 Leu Ser Thr Phe Leu Leu Ile Gly Trp Val Ala Phe Ile Ile Thr Tyr
 450 455 460
 Pro Leu Ser Met His Gln Gln Gln Gln Leu Gln His Gln Gln Phe Gln
 465 470 475 480
 Lys Glu Leu Glu Lys Ile Gln Leu Leu Gln Gln Gln Gln Gln Gln Leu
 485 490 495
 Pro Phe His Pro Pro Gly Asp Thr Ala Gln Asp Gly Glu Leu Leu Asp
 500 505 510

Thr Ser Gly Pro Tyr Ser Glu Ser Ser Gly Thr Ser Ser Pro Ser Thr
 515 520 525
 Ser Pro Arg Ala Ser Asn His Ser Leu Cys Ser Gly Ser Ser Ala Ser
 530 535 540
 Lys Ala Gly Ser Ser Pro Ser Leu Glu Gln Asp Asp Gly Asp Glu Glu
 545 550 555 560
 Thr Ser Val Val Ile Val Gly Lys Ile Ser Phe Cys Pro Lys Asp Val
 565 570 575
 Leu Gly His Gly Ala Glu Gly Thr Ile Val Tyr Arg Gly Met Phe Asp
 580 585 590
 Asn Arg Asp Val Ala Val Lys Arg Ile Leu Pro Glu Cys Phe Ser Phe
 595 600 605
 Ala Asp Arg Glu Val Gln Leu Leu Arg Glu Ser Asp Glu His Pro Asn
 610 615 620
 Val Ile Arg Tyr Phe Cys Thr Glu Lys Asp Arg Gln Phe Gln Tyr Ile
 625 630 635 640

C4
 Comp

Ala Ile Glu Leu Cys Ala Ala Thr Leu Gln Glu Tyr Val Glu Gln Lys
 645 650 655
 Asp Phe Ala His Leu Gly Leu Glu Pro Ile Thr Leu Leu Gln Gln Thr
 660 665 670
 Thr Ser Gly Leu Ala His Leu His Ser Leu Asn Ile Val His Arg Asp
 675 680 685
 Leu Lys Pro His Asn Ile Leu Ile Ser Met Pro Asn Ala His Gly Lys
 690 695 700
 Ile Lys Ala Met Ile Ser Asp Phe Gly Leu Cys Lys Lys Leu Ala Val
 705 710 715 720
 Gly Arg His Ser Phe Ser Arg Arg Ser Gly Val Pro Gly Thr Glu Gly
 725 730 735
 Trp Ile Ala Pro Glu Met Leu Ser Glu Asp Cys Lys Glu Asn Pro Thr
 740 745 750
 Tyr Thr Val Asp Ile Phe Ser Ala Gly Cys Val Phe Tyr Tyr Val Val
 755 760 765
 Ser Glu Gly Ser His Pro Phe Gly Lys Ser Leu Gln Arg Gln Ala Asn
 770 775 780
 Ile Leu Leu Gly Ala Cys Ser Leu Asp Cys Leu His Pro Glu Lys His
 785 790 795 800
 Glu Asp Val Ile Ala Arg Glu Leu Ile Glu Lys Met Ile Ala Met Asp
 805 810 815
 Pro Gln Lys Arg Pro Ser Ala Asn Asp Val Leu Lys His Pro Phe Phe
 820 825 830
 Trp Ser Leu Glu Lys Gln Leu Gln Phe Phe Gln Asp Val Ser Asp Arg
 835 840 845
 Ile Glu Lys Glu Ser Leu Asp Gly Pro Ile Val Lys Gln Leu Glu Arg
 850 855 860
 Gly Gly Arg Ala Val Val Lys Met Asp Trp Arg Glu Asn Ile Thr Asp
 865 870 875 880
 Pro Leu Gln Thr Asp Leu Arg Lys Phe Arg Thr Tyr Lys Gly Gly Ser
 885 890 895
 Val Arg Asp Leu Leu Arg Ala Met Arg Asn Lys Lys His His Tyr Arg
 900 905 910
 Glu Leu Pro Ala Glu Val Arg Glu Thr Leu Gly Thr Leu Pro Asp Asp
 915 920 925
 Phe Val Cys Tyr Phe Thr Ser Arg Phe Pro His Leu Leu Ala His Thr
 930 935 940
 Tyr Arg Ala Met Glu Leu Cys Ser His Glu Arg Leu Phe Gln Pro Tyr
 945 950 955 960

C4
 Cont.

Tyr Phe His Glu Pro Pro Glu Pro Gln Pro Pro Val Thr Pro Asp Ala
 965 970 975

Leu

<210> 3

<211> 983

<212> PRT

<213> Caenorhabditis elegans

<400> 3

Met Arg Ala Thr Phe His Leu Phe Thr Phe Ile Phe Leu Leu Leu Phe
 1 5 10 15

Ser Ser Val Ile Cys Ile Ser Thr Pro Gly Phe Arg Asn Asp His Glu
 20 25 30

Ser Ile Gly Asp Asp Glu Glu Lys Thr Ser Ser Thr Ile Leu Val Ser
 35 40 45

Thr Ile Asp Gly Arg Leu Arg Ala Leu Asp Ser Glu Thr Gly Glu Ile
 50 55 60

Lys Trp Thr Leu Gln Glu Glu Pro Val Leu Arg Ser Pro Ser Ala Val
 65 70 75 80

Lys Gln Gly Phe Thr Phe Leu Pro Asn Pro Leu Asp Gly Ser Leu Tyr
 85 90 95

Val Leu Lys Asn Ser Ser Leu Lys Lys Leu Pro Phe Asn Ile Pro Gln
 100 105 110

Leu Val His Ala Ser Pro Cys Lys Gly Asn Asp Gly Ile Leu Tyr Ala
 115 120 125

Gly Ser Lys Lys Asp Val Trp Phe Gly Ile Asp Pro Lys Thr Gly Leu
 130 135 140

Lys Val Glu Tyr Ile Leu Leu Asn Ile Ser Asp Lys Ile Leu Phe Leu
 145 150 155 160

Gln Val Glu Thr Leu Ser Ser Ala Ser Ala Asp Arg Ile Cys Pro Ala
 165 170 175

Asn Gln Lys Gln Thr Ile Phe Leu Gly Arg Thr Glu Tyr Arg Val Ser
 180 185 190

Met Phe Asp Glu Lys Asn Arg Gly Lys Thr Trp Asn Ala Thr Phe Asn
 195 200 205

Asp Tyr Ser Ala His Leu Leu Pro Glu Val Asn Thr Trp Pro Phe Lys
 210 215 220

His Tyr Ala Ser Ser Ser His Gly Tyr Ile Leu Thr Phe Asp Arg Glu
 225 230 235 240

Thr Gly Glu Met Arg Trp Glu Gln Asp Leu Lys Gln Pro Val Val Ala
 245 250 255

C4
 Cont.

Leu Tyr Leu Leu Arg Asp Asp Gly Leu His Lys Leu Pro Phe Glu Val
 260 265 270
 Met Gly Lys Glu Thr Met Glu Asn Val Ala Lys Asn Ile Phe Thr Val
 275 280 285
 Asp Gln Trp Pro Thr Val Leu Gly Val Asn Ala Ala Asp Pro Gln Thr
 290 295 300
 Thr Ser Leu Thr Asn Gln Phe Phe Pro Ala Leu Phe Val Gly Glu Ser
 305 310 315 320
 Ser Phe Gly Leu Tyr Ala Ile Glu Ala Leu Val Asp His Gln Thr Ile
 325 330 335
 Thr Tyr Ser Pro Lys Leu Leu Gly Pro Pro Leu Leu Glu Gly Pro Ala
 340 345 350
 Pro Ile Ala Leu Thr Glu Met Glu Lys Glu Glu Tyr Leu Pro Pro Arg
 355 360 365
 Arg Pro Ile Ile Arg Asn Ile Pro Pro Ser Ile Thr His Lys Thr Ser
 370 375 380
 Asp Gly Glu Tyr Leu Leu Leu Gly Tyr His Asp Arg Pro Met Met Thr
 385 390 395 400
 Met Ala Thr Ile Ile Pro Thr Arg Tyr Pro Val Pro Gly Pro His Lys
 405 410 415
 Ala Ile Gly Ser Thr Ile Glu Arg Pro Pro Pro Gln Leu Leu Gly Pro
 420 425 430
 Val Glu Pro Gln Lys His Glu Asp Thr Ser Phe Ile Leu Leu Leu Leu
 435 440 445
 Asn Asn His Pro Ile Pro Phe Tyr Ala Thr Leu Val Thr Met Phe Ala
 450 455 460

C4
 Cont

Leu Leu Leu Thr Val Ile Trp Gln Cys Gly Arg Gln Trp Asp Gln Gln
 465 470 475 480
 Lys Ser Thr Ser Arg Met Asp Ser Phe Glu Ile Val Asn Asn Pro Gly
 485 490 495
 Glu Ser Arg Ser Ala Gln Thr Ser Lys Gln Ser Asn Arg Gly Ser Phe
 500 505 510
 Gly Trp Ala Asn Arg Lys Ile Glu Ile Pro Glu Gly Trp Met Ala Val
 515 520 525
 Gly Ser Lys Leu Met Tyr Ser Pro Ser Asp Ile Leu Gly Thr Gly Cys
 530 535 540
 Glu Gly Thr Val Val Tyr Arg Gly Thr Phe Asp Gly Arg Glu Val Ala
 545 550 555 560
 Val Lys Arg Val Val Ser Glu Phe Val Lys Phe Ala His Arg Glu Ala
 565 570 575
 Asp Leu Leu Arg Glu Ser Asp Thr His Pro His Val Ile Arg Tyr Phe

580	585	590
Cys Met Glu Ser Asp Ser Gln Phe Arg Tyr Leu Ala Leu Glu Leu Cys 595	600	605
Ile Ala Ser Leu Asn Asp Tyr Val Glu Gln Lys Glu Val Gln Gln Asn 610	615	620
Val Thr Ile Ala Leu Arg Asp Ile Met Lys Gln Ala Thr Asp Gly Leu 625	630	635
Ala His Leu His Ala Ser Lys Ile Val His Arg Asp Met Lys Pro Gln 645	650	655
Asn Val Leu Ile Thr Met Ala Ser Gln Arg Gly Glu Met Arg Ala Val 660	665	670
Ile Ser Asp Phe Gly Leu Cys Lys Arg Val Gln Pro Gly Lys Asn Ser 675	680	685
Ile Ser Arg Gly Ile Ala Ser Gly Leu Ala Gly Thr Asp Gly Trp Ile 690	695	700
Ala Pro Glu Val Leu Ile Ser Ala Ser Thr Ser Tyr Pro Val Asp Ile 705	710	715
Phe Ser Leu Gly Cys Ile Phe Tyr Tyr Val Leu Thr Ser Gly Thr His 725	730	735
Pro Phe Gly Lys Ser Leu His Arg Gln Ala Asn Ile Val Asn Gly Glu 740	745	750
Tyr Thr Leu Asn Lys Leu Ala Asp Leu Asp Asp Trp Ser Leu Ala Asp 755	760	765
Asp Leu Ile Ser Ser Met Leu Asn Val Glu Pro Leu His Arg Leu Thr 770	775	780

Ala Asp Ala Val Leu Asn His Pro Phe Phe Trp Thr Ser Glu Lys Arg 785	790	795	800
Leu Ala Tyr Phe Ser Asp Val Ser Asp Arg Val Glu Lys Glu Glu Asp 805	810	815	
Asn Ser Pro Val Val Arg Arg Ile Glu Thr Asp Ala Arg Ile Val Val 820	825	830	
Cys Gly Gly Trp Arg Glu Lys Ile Cys Asp Ala Leu Lys Glu Asp Leu 835	840	845	
Arg Lys Phe Arg Thr Tyr Lys Ser Phe Ser Val Arg Asp Leu Leu Arg 850	855	860	
Ala Met Arg Asn Lys Lys His His Tyr Arg Glu Leu Pro Glu Asp Val 865	870	875	880
Arg Gln Ser Leu Gly Asp Ile Pro Asp Gln Phe Leu His Tyr Phe Thr 885	890	895	
Ser Arg Phe Pro Arg Leu Leu Leu His Val Tyr Lys Ala Thr Glu Tyr 900	905	910	

C4
Cont

Cys Ser Gly Glu Ala Val Phe Lys Arg Tyr Tyr Ser Asp Asp Val Arg
 915 920 925

Ala Arg Met Tyr Pro Ile Val Glu Glu Glu Glu Arg Val Arg Lys Lys
 930 935 940

Ile Lys Glu Glu Met Ala Asn Glu Val Trp Ala Arg Ala Pro Lys Pro
 945 950 955 960

Val Glu Gln Arg Thr Pro Leu Lys Leu Asp Lys Arg Asn Ile Lys Lys
 965 970 975

Lys Ser Asn Pro Asn Thr Asp
 980

<210> 4

<211> 443

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 4

Leu Val Val Ser Cys Lys Ile Leu Gly Tyr Gly Ser Ser Gly Thr Val
 1 5 10 15

Val Phe Gln Gly Ser Phe Gln Gly Arg Pro Val Ala Val Lys Arg Met
 20 25 30

Leu Ile Asp Phe Cys Asp Ile Ala Leu Met Glu Ile Lys Leu Leu Thr
 35 40 45

Glu Ser Asp Asp His Pro Asn Val Ile Arg Tyr Tyr Cys Ser Glu Thr
 50 55 60

Thr Asp Arg Phe Leu Tyr Ile Ala Leu Glu Leu Cys Asn Leu Asn Leu
 65 70 75 80

Gln Asp Leu Val Glu Ser Lys Asn Val Ser Asp Glu Asn Leu Lys Leu
 85 90 95

Gln Lys Glu Tyr Asn Pro Ile Ser Leu Leu Arg Gln Ile Ala Ser Gly
 100 105 110

Val Ala His Leu His Ser Leu Lys Ile Ile His Arg Asp Leu Lys Pro
 115 120 125

Gln Asn Ile Leu Val Ser Thr Ser Ser Arg Phe Thr Ala Asp Gln Gln
 130 135 140

Thr Gly Ala Glu Asn Leu Arg Ile Leu Ile Ser Asp Phe Gly Leu Cys
 145 150 155 160

Lys Lys Leu Asp Ser Gly Gln Ser Ser Phe Arg Thr Asn Leu Asn Asn
 165 170 175

Pro Ser Gly Thr Ser Gly Trp Arg Ala Pro Glu Leu Leu Glu Glu Ser
 180 185 190

Asn Asn Leu Gln Cys Gln Val Glu Thr Glu His Ser Ser Ser Arg His
 195 200 205

C4
 Cont

Thr Val Val Ser Ser Asp Ser Phe Tyr Asp Pro Phe Thr Lys Arg Arg
 210 215 220
 Leu Thr Arg Ser Ile Asp Ile Phe Ser Met Gly Cys Val Phe Tyr Tyr
 225 230 235 240
 Ile Leu Ser Lys Gly Lys His Pro Phe Gly Asp Lys Tyr Ser Arg Glu
 245 250 255
 Ser Asn Ile Ile Arg Gly Ile Phe Ser Leu Asp Glu Met Lys Cys Leu
 260 265 270
 His Asp Arg Ser Leu Ile Ala Glu Ala Thr Asp Leu Ile Ser Gln Met
 275 280 285
 Ile Asp His Asp Pro Leu Lys Arg Pro Thr Ala Met Lys Val Leu Arg
 290 295 300
 His Pro Leu Phe Trp Pro Lys Ser Lys Lys Leu Glu Phe Leu Leu Lys
 305 310 315 320
 Val Ser Asp Arg Leu Glu Ile Glu Asn Arg Asp Pro Pro Ser Ala Leu
 325 330 335
 Leu Met Lys Phe Asp Ala Gly Ser Asp Phe Val Ile Pro Ser Gly Asp
 340 345 350
 Trp Thr Val Lys Phe Asp Lys Thr Phe Met Asp Asn Leu Glu Arg Tyr
 355 360 365
 Arg Lys Tyr His Ser Ser Lys Leu Met Asp Leu Leu Arg Ala Leu Arg
 370 375 380
 Asn Lys Tyr His His Phe Met Asp Leu Pro Glu Asp Ile Ala Glu Leu
 385 390 395 400
~~Met Gly Pro Val Pro Asp Gly Phe Tyr Asp Tyr Phe Thr Lys Arg Phe~~
~~405 410 415~~
 Pro Asn Leu Leu Ile Gly Val Tyr Met Ile Val Lys Glu Asn Leu Ser
 420 425 430
 Asp Asp Gln Ile Leu Arg Glu Phe Leu Tyr Ser
 435 440

<210> 5

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 5

Ile Ser Asp Phe Gly Leu Cys Lys

1

5

<210> 6

C4
Cont

<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 6
cgccatgcc

9

<210> 7
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> 1
<223> N may be Thymine or Cytosine

<220>
<221> misc_feature
<222> 4,9,13,16
<223> N may be Adenine or Guanine

<220>
<221> misc_feature
<222> 7,10,19,22
<223> N may be any nucleotide

<220>
<221> misc_feature
<222> 21
<223> N may be Adenine or Thymine

<220>
<223> Description of Artificial Sequence: Primer

<400> 7
nttncntntnn ccnaantcng nnat

24

<210> 8
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 8
Ile Ser Asp Phe Gly Leu Cys Lys
1 5

<210> 9
<211> 28
<212> DNA
<213> Artificial Sequence

C4
Cont

<220>

<223> Description of Artificial Sequence: Primer

<400> 9

gctctagaac catgccggcc cggcggct

28

<210> 10

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 10

aggctgccat cattaggatc t

21

<210> 11

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 11

cattgatgtg catcaccttc ctc

23

<210> 12

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 12

cggaattcat cacctatccc ctgagcatg

29

<210> 13

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 13

cggaattctc agagggcgctc tggagtca

28

C4
Cont